

SEQUENCE LISTING

<110> University of Bristol

<120> Novel method for the production of polyunsaturated
fatty acids

<130> 2002_791

<140> 2002_271

<141> 2202-12-18

<160> 10

<170> PatentIn Ver. 2.0

<210> 1

<211> 1266

<212> DNA

<213> *Euglena gracilis*

<220>

<221> CDS

<222> (1)..(1266)

<223> delta-8-desaturase

<400> 1

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Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr

1 5 10 15

tat gat gtg tct gcc tgg gtc aat ttc cac cct ggt ggt gcg gaa att 96

Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile

20 25 30

ata gag aat tac caa gga agg gat gcc act gat gcc ttc atg gtt atg 144

Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
 35 40 45

cac tct caa gaa gcc ttc gac aag ctc aag cgc atg ccc aaa atc aat 192
 His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
 50 55 60

ccc agt tct gag ttg cca ccc cag gct gca gtg aat gaa gct caa gag 240
 Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
 65 70 75 80

gat ttc cgg aag ctc cga gaa gag ttg atc gca act ggc atg ttt gat 288
 Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
 85 90 95

gcc tcc ccc ctc tgg tac tca tac aaa atc agc acc aca ctg ggc ctt 336
 Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
 100 105 110

gga gtg ctg ggt tat ttc ctg atg gtt cag tat cag atg tat ttc att 384
 Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
 115 120 125

ggg gca gtg ttg ctt ggg atg cac tat caa cag atg ggc tgg ctt tct 432
 Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
 130 135 140

cat gac att tgc cac cac cag act ttc aag aac cgg aac tgg aac aac 480
 His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
 145 150 155 160

ctc gtg gga ctg gta ttt ggc aat ggt ctg caa ggt ttt tcc gtg aca 528
 Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
 165 170 175

tgc tgg aag gac aga cac aat gca cat cat tcg gca acc aat gtt caa	576
Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln	
180 185 190	
ggg cac gac cct gat att gac aac ctc ccc ctc tta gcc tgg tct gag	624
Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu	
195 200 205	
gat gac gtc aca cgg gcg tca ccg att tcc cgc aag ctc att cag ttc	672
Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe	
210 215 220	
cag cag tat tat ttc ttg gtc atc tgt atc ttg ttg cgg ttc att tgg	720
Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp	
225 230 235 240	
tgt ttc cag agc gtg ttg acc gtg cgc agt ctg aag gac aga gat aac	768
Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn	
245 250 255	
caa ttc tat cgc tct cag tat aag aag gag gcc att ggc ctc gcc ctg	816
Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu	
260 265 270	
cat tgg aca ttg aag gcc ctg ttc cac tta ttc ttt atg ccc agc atc	864
His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile	
275 280 285	
ctc aca tcg ctg ttg gta ttt ttc gtt tcg gag ctg gtt ggc ggc ttc	912
Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe	
290 295 300	
ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc	960
Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile	
305 310 315 320	

ggg gac tcg gtc tgg gat ggc cat gga ttc tcg gtt ggc cag atc cat 1008
Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
325 330 335

gag acc atg aac att cgg cga ggg att atc aca gat tgg ttt ttc gga 1056
Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
340 345 350

ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc 1104
Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
355 360 365

cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag 1152
His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
370 375 380

cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc 1200
His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
385 390 395 400

ctg ctg cgc tat ctg gcg gtg ttc gcc cgg atg gcg gag aag caa ccc 1248
Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
405 410 415

gcg ggg aag gct cta taa 1266
Ala Gly Lys Ala Leu
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<210> 2

<211> 421

<212> PRT

<213> Euglena gracilis

<400> 2

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Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile

20 25 30

Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met

35 40 45

His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn

50 55 60

Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu

65 70 75 80

Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp

85 90 95

Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu

100 105 110

Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile

115 120 125

Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser

130 135 140

His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn

145 150 155 160

Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr

165 170 175

Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln

6/30

180	185	190
Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu		
195	200	205
Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe		
210	215	220
Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp		
225	230	235
		240
Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn		
245	250	255
Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu		
260	265	270
His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile		
275	280	285
Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe		
290	295	300
Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile		
305	310	315
		320
Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His		
325	330	335
Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly		
340	345	350
Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg		
355	360	365

His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys

370

375

380

His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile

385

390

395

400

Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro

405

410

415

Ala Gly Lys Ala Leu

420

<210> 3

<211> 777

<212> DNA

<213> Isochrysis galbana

<220>

<221> CDS

<222> (1)..(777)

<223> delta-9-elongase

<400> 3

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10

15

gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg 96

Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro

20

25

30

ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg 144

Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg

35

40

45

acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg 192
 Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
 50 55 60

agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc 240
 Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
 65 70 75 80

gcg tgg ctg cgc agg caa acc gcc gac aca ccg cag ccg ctc ttc cag 288
 Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
 85 90 95

tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag 336
 Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
 100 105 110

gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg 384
 Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
 115 120 125

agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat 432
 Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
 130 135 140

gtg tac ctc gcc att cgg ctg cac aac gag ggc gta tgg atc ttc atg 480
 Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
 145 150 155 160

ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc 528
 Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu
 165 170 175

acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg 576
 Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met

180

185

190

cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc 624
 Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile
 195 200 205

aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct 672
 Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala
 210 215 220

ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt 720
 Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
 225 230 235 240

ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag 768
 Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys
 245 250 255

cag ctc tag 777
 Gln Leu

<210> 4

<211> 258

<212> PRT

<213> Isochrysis galbana

<400> 4

Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr
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Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
 20 25 30

Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg

10/30

35	40	45
Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu		
50	55	60
Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly		
65	70	75
80		
Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln		
85	90	95
Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys		
100	105	110
Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu		
115	120	125
Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp		
130	135	140
Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met		
145	150	155
160		
Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu		
165	170	175
Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met		
180	185	190
Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile		
195	200	205
Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala		
210	215	220

11/30

Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
 225 230 235 240

Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys
 245 250 255

Gln Leu

<210> 5

<211> 1410

<212> DNA

<213> *Phaeodactylum tricornutum*

<220>

<221> CDS

<222> (1)..(1410)

<223> delta-5-desaturase

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 Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val
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gcg aag cac aat gct gct acc ata tcg acg cag gaa cgc ctt tgc agt 96
 Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser
 20 25 30

ctg tct tcg ctc aaa ggc gaa gaa gtc tgc atc gac gga atc atc tat 144
 Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr
 35 40 45

gac ctc caa tca ttc gat cat ccc ggg ggt gaa acg atc aaa atg ttt 192
 Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe
 50 55 60

ggt ggc aac gat gtc act gta cag tac aag atg att cac ccg tac cat 240
 Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His
 65 70 75 80

acc gag aag cat ttg gaa aag atg aag cgt gtc ggc aag gtg acg gat 288
 Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp
 85 90 95

ttc gtc tgc gag tac aag ttc gat acc gaa ttt gaa cgc gaa atc aaa 336
 Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys
 100 105 110

cga gaa gtc ttc aag att gtg cga cga ggc aag gat ttc ggt act ttg 384
 Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu
 115 120 125

gga tgg ttc ttc cgt gcg ttt tgc tac att gcc att ttc ttc tac ctg 432
 Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu
 130 135 140

cag tac cat tgg gtc acc acg gga acc tct tgg ctg ctg gcc gtg gcc 480
 Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala
 145 150 155 160

tac gga atc tcc caa gcg atg att ggc atg aat gtc cag cac gat gcc 528
 Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala
 165 170 175

aac cac ggg gcc acc tcc aag cgt ccc tgg gtc aac gac atg cta ggc 576
 Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly
 180 185 190

ctc ggt gcg gat ttt att ggt ggt tcc aag tgg ctc tgg cag gaa caa 624
 Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln

195	200	205	
cac tgg acc cac cac gct tac acc aat cac gcc gag atg gat ccc gat			672
His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp			
210	215	220	
agc ttt ggt gcc gaa cca atg ctc cta ttc aac gac tat ccc ttg gat			720
Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp			
225	230	235	240
cat ccc gct cgt acc tgg cta cat cgc ttt caa gca ttc ttt tac atg			768
His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met			
	245	250	255
ccc gtc ttg gct gga tac tgg ttg tcc gct gtc ttc aat cca caa att			816
Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile			
	260	265	270
ctt gac ctc cag caa cgc ggc gca ctt tcc gtc ggt atc cgt ctc gac			864
Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp			
	275	280	285
aac gct ttc att cac tcg cga cgc aag tat gcg gtt ttc tgg cgg gct			912
Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala			
	290	295	300
gtg tac att gcg gtg aac gtg att gct cgg ttt tac aca aac tcc ggc			960
Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly			
305	310	315	320
ctc gaa tgg tcc tgg cgt gtc ttt gga aac atc atg ctc atg ggt gtg			1008
Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val			
	325	330	335
gcg gaa tcg ctc gcg ctg gcg gtc ctg ttt tcg ttg tcg cac aat ttc			1056

Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe	
340	345 350
gaa tcc gcg gat cgc gat ccg acc gcc cca ctg aaa aag acg gga gaa	1104
Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu	
355	360 365
cca gtc gac tgg ttc aag aca cag gtc gaa act tcc tgc act tac ggt	1152
Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly	
370	375 380
gga ttc ctt tcc ggt tgc ttc acg gga ggt ctc aac ttt cag gtt gaa	1200
Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu	
385	390 395 400
cac cac ttg ttc cca cgc atg agc agc gct tgg tat ccc tac att gcc	1248
His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala	
405	410 415
ccc aag gtc cgc gaa att tgc gcc aaa cac gcc gtc cac tac gcc tac	1296
Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr	
420	425 430
tac ccg tgg atc cac caa aac ttt ctc tcc acc gtc cgc tac atg cac	1344
Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His	
435	440 445
gcg gcc ggg acc ggt gcc aac tgg cgc cag atg gcc aga gaa aat ccc	1392
Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro	
450	455 460
ttg acc gga cgg gcg taa	1410
Leu Thr Gly Arg Ala	
465	470

<210> 6

<211> 469

<212> PRT

<213> *Phaeodactylum tricornutum*

<400> 6

Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val
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Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser
20 25 30

Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr
35 40 45

Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe
50 55 60

Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His
65 70 75 80

Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp
85 90 95

Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys
100 105 110

Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu
115 120 125

Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu
130 135 140

Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala

16/30

145	150	155	160
Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala			
165	170	175	
Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly			
180	185	190	
Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln			
195	200	205	
His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp			
210	215	220	
Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp			
225	230	235	240
His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met			
245	250	255	
Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile			
260	265	270	
Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp			
275	280	285	
Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala			
290	295	300	
Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly			
305	310	315	320
Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val			
325	330	335	

17/30

Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe

340

345

350

Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu

355

360

365

Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly

370

375

380

Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu

385

390

395

400

His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala

405

410

415

Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr

420

425

430

Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His

435

440

445

Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro

450

455

460

Leu Thr Gly Arg Ala

465

<210> 7

<211> 1344

<212> DNA

<213> Ceratodon purpureus

<220>

<221> CDS

<222> (1)..(1344)

<223> delta-5-desaturase

<400> 7

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gga aaa tgg tgt caa att gac gat gct gtc ctg aga tca cat cca ggt 96

Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly

20 25 30

ggg agt gca att act acc tat aaa aat atg gat gcc act acc gta ttc 144

Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe

35 40 45

cac aca ttc cat act ggt tct aaa gaa gcg tat caa tgg ctg aca gaa 192

His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu

50 55 60

ttg aaa aaa gag tgc cct aca caa gaa cca gag atc cca gat att aag 240

Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys

65 70 75 80

gat gac cca atc aaa gga att gat gat gtg aac atg gga act ttc aat 288

Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn

85 90 95

att tct gag aaa cga tct gcc caa ata aat aaa agt ttc act gat cta 336

Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu

100 105 110

cgt atg cga gtt cgt gca gaa gga ctt atg gat gga tct cct ttg ttc 384

Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe

115 120 125

tac att aga aaa att ctt gaa aca atc ttc aca att ctt ttt gca ttc 432
 Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe
 130 135 140

tac ctt caa tac cac aca tat tat ctt cca tca gct att cta atg gga 480
 Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly
 145 150 155 160

gtt gcg tgg caa caa ttg gga tgg tta atc cat gaa ttc gca cat cat 528
 Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His
 165 170 175

cag ttg ttc aaa aac aga tac tac aat gat ttg gcc agc tat ttc gtt 576
 Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val
 180 185 190

gga aac ttt tta caa gga ttc tca tct ggt ggt tgg aaa gag cag cac 624
 Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His
 195 200 205

aat gtg cat cac gca gcc aca aat gtt gtt gga cga gac gga gat ctt 672
 Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu
 210 215 220

gat tta gtc cca ttc tat gct aca gtg gca gaa cat ctc aac aat tat 720
 Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr
 225 230 235 240

tct cag gat tca tgg gtt atg act cta ttc aga tgg caa cat gtt cat 768
 Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His
 245 250 255

tgg aca ttc atg tta cca ttc ctc cgt ctc tcg tgg ctt ctt cag tca 816
 Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser

260	265	270	
atc att ttt gtt agt cag atg cca act cat tat tat gac tat tac aga			864
Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg			
275	280	285	
aat act gcg att tat gaa cag gtt ggt ctc tct ttg cac tgg gct tgg			912
Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp			
290	295	300	
tca ttg ggt caa ttg tat ttc cta ccc gat tgg tca act aga ata atg			960
Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met			
305	310	315	320
ttc ttc ctt gtt tct cat ctt gtt gga ggt ttc ctg ctc tct cat gta			1008
Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val			
325	330	335	
gtt act ttc aat cat tat tca gtg gag aag ttt gca ttg agc tcg aac			1056
Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn			
340	345	350	
atc atg tca aat tac gct tgt ctt caa atc atg acc aca aga aat atg			1104
Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met			
355	360	365	
aga cct gga aga ttc att gac tgg ctt tgg gga ggt ctt aac tat cag			1152
Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln			
370	375	380	
att gag cac cat ctt ttc cca acg atg cca cga cac aac ttg aac act			1200
Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr			
385	390	395	400
gtt atg cca ctt gtt aag gag ttt gca gca gca aat ggt tta cca tac			1248

Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr
 405 410 415

atg gtc gac gat tat ttc aca gga ttc tgg ctt gaa att gag caa ttc 1296
 Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe
 420 425 430

cga aat att gca aat gtt gct gct aaa ttg act aaa aag att gcc tag 1344
 Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala
 435 440 445

<210> 8

<211> 447

<212> PRT

<213> Ceratodon purpureus

<400> 8

Met Val Leu Arg Glu Gln Glu His Glu Pro Phe Phe Ile Lys Ile Asp
 1 5 10 15

Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly
 20 25 30

Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe
 35 40 45

His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu
 50 55 60

Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys
 65 70 75 80

Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn
 85 90 95

Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu
100 105 110

Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe
115 120 125

Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe
130 135 140

Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly
145 150 155 160

Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His
165 170 175

Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val
180 185 190

Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His
195 200 205

Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu
210 215 220

Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr
225 230 235 240

Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His
245 250 255

Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser
260 265 270

Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg

275

280

285

Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp
290 295 300

Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met
305 310 315 320

Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val
325 330 335

Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn
340 345 350

Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met
355 360 365

Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln
370 375 380

Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr
385 390 395 400

Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr
405 410 415

Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe
420 425 430

Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala
435 440 445

<210> 9

<211> 1443

<212> DNA

<213> *Physcomitrella patens*

<220>

<221> CDS

<222> (1)..(1443)

<223> delta-5-desaturase

<400> 9

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Met Ala Pro His Ser Ala Asp Thr Ala Gly Leu Val Pro Ser Asp Glu

1 5 10 15

ttg agg cta cga acg tcg aat tca aag ggt ccc gaa caa gag caa act 96

Leu Arg Leu Arg Thr Ser Asn Ser Lys Gly Pro Glu Gln Glu Gln Thr

20 25 30

ttg aag aag tac acc ctt gaa gat gtc agc cgc cac aac acc cca gca 144

Leu Lys Lys Tyr Thr Leu Glu Asp Val Ser Arg His Asn Thr Pro Ala

35 40 45

gat tgt tgg ttg gtg ata tgg ggc aaa gtc tac gat gtc aca agc tgg 192

Asp Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val Thr Ser Trp

50 55 60

att ccc aat cat ccg ggg ggc agt ctc atc cac gta aaa gca ggg cag 240

Ile Pro Asn His Pro Gly Gly Ser Leu Ile His Val Lys Ala Gly Gln

65 70 75 80

gat tcc act cag ctt ttc gat tcc tat cac ccc ctt tat gtc agg aaa 288

Asp Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr Val Arg Lys

85 90 95

atg ctc gcg aag tac tgt att ggg gaa tka gta ccg tct gct ggt gat 336

Met Leu Ala Lys Tyr Cys Ile Gly Glu Xaa Val Pro Ser Ala Gly Asp

100	105	110	
gac aag ttt aag aaa gca act ctg rag tat gca gat gcc gaa aat gaa			384
Asp Lys Phe Lys Lys Ala Thr Leu Xaa Tyr Ala Asp Ala Glu Asn Glu			
115	120	125	
gat ttc tat ttg gtt gtg aag caa cga gtt gaa tct tat ttc aag agt			432
Asp Phe Tyr Leu Val Val Lys Gln Arg Val Glu Ser Tyr Phe Lys Ser			
130	135	140	
aac aag ata aac ccc caa att cat cca cat atg atc ctg aag tca ttg			480
Asn Lys Ile Asn Pro Gln Ile His Pro His Met Ile Leu Lys Ser Leu			
145	150	155	160
ttc att ctt ggg gga tat ttc gcc agt tac tat tta gcg ttc ttc tgg			528
Phe Ile Leu Gly Gly Tyr Phe Ala Ser Tyr Tyr Leu Ala Phe Phe Trp			
165	170	175	
tct tca agt gtc ctt gtt tct ttg ttt ttc gca ttg tgg atg ggg ttc			576
Ser Ser Ser Val Leu Val Ser Leu Phe Phe Ala Leu Trp Met Gly Phe			
180	185	190	
ttc gca gcg gaa gtc ggc gtg tcg att caa cat gat gga aat cat ggt			624
Phe Ala Ala Glu Val Gly Val Ser Ile Gln His Asp Gly Asn His Gly			
195	200	205	
tca tac act aaa tgg cgt ggc ttt gga tat atc atg gga gcc tcc cta			672
Ser Tyr Thr Lys Trp Arg Gly Phe Gly Tyr Ile Met Gly Ala Ser Leu			
210	215	220	
gat cta gtc gga gcc agt agc ttc atg tgg aga cag caa cac gtt gtg			720
Asp Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln His Val Val			
225	230	235	240
gga cat cac tcg ttt aca aat gtg gac aac tac gat cct gat att cgt			768

Gly His His Ser Phe Thr Asn Val Asp Asn Tyr Asp Pro Asp Ile Arg	
245	250 255
gtg aaa gat cca gat gtc agg agg gtt gcg acc aca caa cca aga caa	816
Val Lys Asp Pro Asp Val Arg Arg Val Ala Thr Thr Gln Pro Arg Gln	
260	265 270
tgg tat cat gcg tat cag cat atc tac ctg gca gta tta tat gga act	864
Trp Tyr His Ala Tyr Gln His Ile Tyr Leu Ala Val Leu Tyr Gly Thr	
275	280 285
cta gct ctt aag agt att ttt cta gat gat ttc ctt gcg tac ttc aca	912
Leu Ala Leu Lys Ser Ile Phe Leu Asp Asp Phe Leu Ala Tyr Phe Thr	
290	295 300
gga tca att ggc cct gtc aag gtg gcg aaa atg acc ccc ctg gag ttc	960
Gly Ser Ile Gly Pro Val Lys Val Ala Lys Met Thr Pro Leu Glu Phe	
305	310 315 320
aac atc ttc ttt cag gga aag ctg cta tat gcg ttc tac atg ttc gtg	1008
Asn Ile Phe Phe Gln Gly Lys Leu Leu Tyr Ala Phe Tyr Met Phe Val	
325	330 335
ttg cca tct gtg tac ggt gtt cac tcc gga gga act ttc ttg gca cta	1056
Leu Pro Ser Val Tyr Gly Val His Ser Gly Gly Thr Phe Leu Ala Leu	
340	345 350
tat gtg gct tct cag ctc att aca ggt tgg atg tta gct ttt ctt ttt	1104
Tyr Val Ala Ser Gln Leu Ile Thr Gly Trp Met Leu Ala Phe Leu Phe	
355	360 365
caa gta gca cat gtc gtg gat gat gtt gca ttt cct aca cca gaa ggt	1152
Gln Val Ala His Val Val Asp Asp Val Ala Phe Pro Thr Pro Glu Gly	
370	375 380

27/30

ggg aag gtg aag gga gga tgg gct gca atg cag gtt gca aca act acg 1200
Gly Lys Val Lys Gly Gly Trp Ala Ala Met Gln Val Ala Thr Thr Thr
385 390 395 400

gat ttc agt cca cgc tca tgg ttc tgg ggt cat gtc tct gga gga tta 1248
Asp Phe Ser Pro Arg Ser Trp Phe Trp Gly His Val Ser Gly Gly Leu
405 410 415

aac aac caa att gag cat cat ctg ttt cca gga gtg tgc cat gtt cat 1296
Asn Asn Gln Ile Glu His His Leu Phe Pro Gly Val Cys His Val His
420 425 430

tat cca gcc att cag cct att gtc gag aag acg tgc aag gaa ttc gat 1344
Tyr Pro Ala Ile Gln Pro Ile Val Glu Lys Thr Cys Lys Glu Phe Asp
435 440 445

gtg cct tat gta gcc tac cca act ttt tgg act gcg ttg aga gcc cac 1392
Val Pro Tyr Val Ala Tyr Pro Thr Phe Trp Thr Ala Leu Arg Ala His
450 455 460

ttt gcg cat ttg aaa aag gtt gga ttg aca gag ttt cgg ctc gat ggc 1440
Phe Ala His Leu Lys Lys Val Gly Leu Thr Glu Phe Arg Leu Asp Gly
465 470 475 480

tga 1443

<210> 10

<211> 480

<212> PRT

<213> Physcomitrella patens

<400> 10

Met Ala Pro His Ser Ala Asp Thr Ala Gly Leu Val Pro Ser Asp Glu

28/30

1	5	10	15
Leu Arg Leu Arg Thr Ser Asn Ser Lys Gly Pro Glu Gln Glu Gln Thr			
20	25	30	
Leu Lys Lys Tyr Thr Leu Glu Asp Val Ser Arg His Asn Thr Pro Ala			
35	40	45	
Asp Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val Thr Ser Trp			
50	55	60	
Ile Pro Asn His Pro Gly Gly Ser Leu Ile His Val Lys Ala Gly Gln			
65	70	75	80
Asp Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr Val Arg Lys			
85	90	95	
Met Leu Ala Lys Tyr Cys Ile Gly Glu Xaa Val Pro Ser Ala Gly Asp			
100	105	110	
Asp Lys Phe Lys Lys Ala Thr Leu Xaa Tyr Ala Asp Ala Glu Asn Glu			
115	120	125	
Asp Phe Tyr Leu Val Val Lys Gln Arg Val Glu Ser Tyr Phe Lys Ser			
130	135	140	
Asn Lys Ile Asn Pro Gln Ile His Pro His Met Ile Leu Lys Ser Leu			
145	150	155	160
Phe Ile Leu Gly Gly Tyr Phe Ala Ser Tyr Tyr Leu Ala Phe Phe Trp			
165	170	175	
Ser Ser Ser Val Leu Val Ser Leu Phe Phe Ala Leu Trp Met Gly Phe			
180	185	190	

29/30

Phe Ala Ala Glu Val Gly Val Ser Ile Gln His Asp Gly Asn His Gly

195

200

205

Ser Tyr Thr Lys Trp Arg Gly Phe Gly Tyr Ile Met Gly Ala Ser Leu

210

215

220

Asp Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln His Val Val

225

230

235

240

Gly His His Ser Phe Thr Asn Val Asp Asn Tyr Asp Pro Asp Ile Arg

245

250

255

Val Lys Asp Pro Asp Val Arg Arg Val Ala Thr Thr Gln Pro Arg Gln

260

265

270

Trp Tyr His Ala Tyr Gln His Ile Tyr Leu Ala Val Leu Tyr Gly Thr

275

280

285

Leu Ala Leu Lys Ser Ile Phe Leu Asp Asp Phe Leu Ala Tyr Phe Thr

290

295

300

Gly Ser Ile Gly Pro Val Lys Val Ala Lys Met Thr Pro Leu Glu Phe

305

310

315

320

Asn Ile Phe Phe Gln Gly Lys Leu Leu Tyr Ala Phe Tyr Met Phe Val

325

330

335

Leu Pro Ser Val Tyr Gly Val His Ser Gly Gly Thr Phe Leu Ala Leu

340

345

350

Tyr Val Ala Ser Gln Leu Ile Thr Gly Trp Met Leu Ala Phe Leu Phe

355

360

365

Gln Val Ala His Val Val Asp Asp Val Ala Phe Pro Thr Pro Glu Gly

370

375

380

Gly Lys Val Lys Gly Gly Trp Ala Ala Met Gln Val Ala Thr Thr Thr
385 390 395 400

Asp Phe Ser Pro Arg Ser Trp Phe Trp Gly His Val Ser Gly Gly Leu
405 410 415

Asn Asn Gln Ile Glu His His Leu Phe Pro Gly Val Cys His Val His
420 425 430

Tyr Pro Ala Ile Gln Pro Ile Val Glu Lys Thr Cys Lys Glu Phe Asp
435 440 445

Val Pro Tyr Val Ala Tyr Pro Thr Phe Trp Thr Ala Leu Arg Ala His
450 455 460

Phe Ala His Leu Lys Lys Val Gly Leu Thr Glu Phe Arg Leu Asp Gly
465 470 475 480